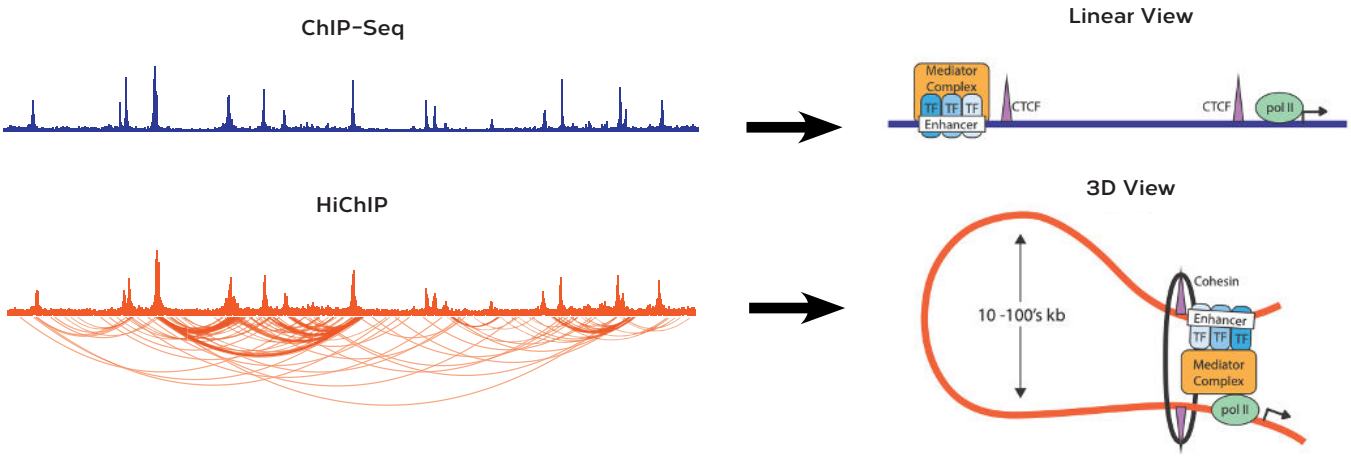
Get The Most Of Your ChIP-seq Experiments

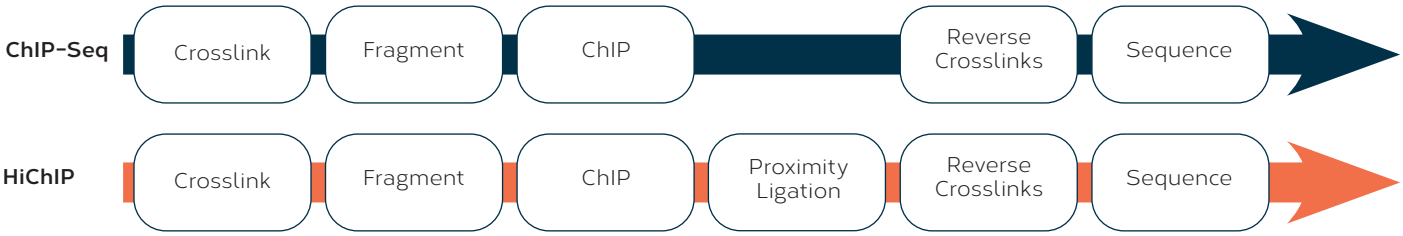
By Capturing The Protein Interactome

The Dovetail® HiChIP MNase Kit combines the benefits of ChIP-seq with Hi-C, a proximity ligation method that captures long-range interactions using standard Illumina paired-end sequencing. Query protein-directed chromatin conformation mediated by specific proteins of interest and see your ChIP-seq data in a whole new dimension.

See Your ChIP-Seq Data In A Whole New Dimension



Adding A Proximity-Ligation Step To Your ChIP-Seq Work Enables You To Assess The Protein-Directed Chromatin Interactome



Genomic interactions matter. With ChIP-seq, you only get chromatin information in linear space – meaning you may not be getting all the details you need to gain insights on how enhancer/promoter interactions and protein-directed chromatin architecture regulates gene expression. HiChIP gives your ChIP-seq data a 3D boost so you can take your data to new dimensions. Use conformation contact information to explore how regulatory elements and the spatial relationships between regulatory elements can influence gene expression and drive disease progression.

Target	CTCF	H3Kac27 or H3K4me	Transcription Factor
ChIP-Seq	• Find putative chromatin boundaries	• Find enhancers sites • Identify active promoters	• Locate binding sites • Find nearest-neighbor promoters
HiChIP	• **Classify** role of each CTCF site • **Assign** chromatin boundaries • **Identify** TAD and loop anchors	• **Classify** super-enhancers • **Find** yet to be described E-P interactions • **Annotate** the enhancer to correct the target promoter(s)	• **Determine** the regions of highest interactions • **Discover** new regions outside the TF footprint to investigate

Aging Driven By Distal Enhancers

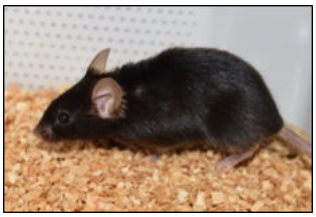
Data courtesy of Sinclair Lab, Harvard University

Does the response to DNA breakage induce changes in chromatin that drive aging?

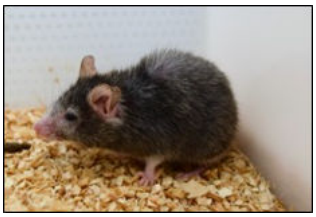
ICE mice (inducible changes to the epigenome)

Cells derived from ICE mice

Double Stranded DNA Breaks (DBS) Induces Premature Aging



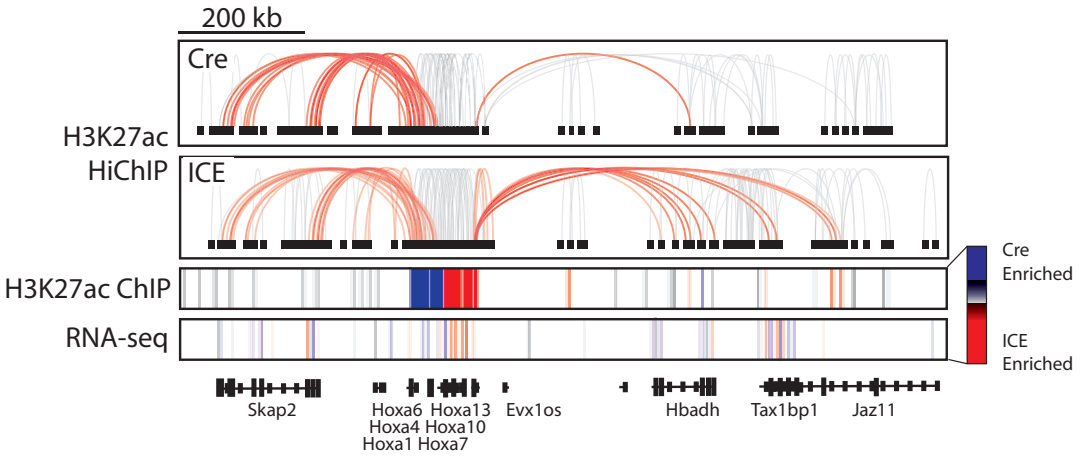
Cre



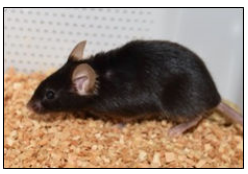
ICE

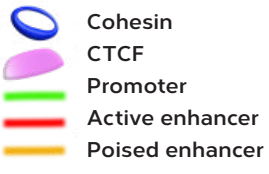
Both mice are 16 months old, the treated specimen (subjected to DBS at 6 months) displays signs of aging such as grey hair, and spine curvature

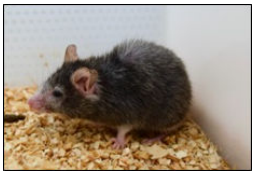
Results: The HoxA cluster in older mice display an increase of interactions with distal enhancers. While there are local changes in enhancer marks at the HoxA cluster between Cre and ICE samples, the ICE interactome is enriched with long-range engagement with ICE-specific enhancer marks many 100's of kb downstream.

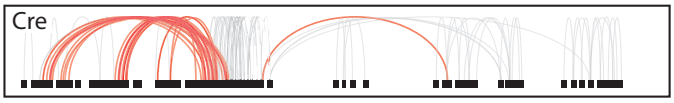


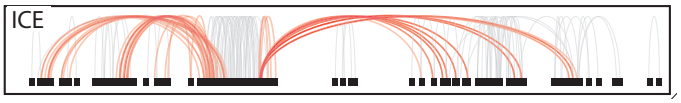
Conclusion: Repairs to double stranded DNA breaks in ICE mice leads to the alteration of chromatin structure, by introducing new enhancer regions and changes in the interactome leading to abnormal expression Hox.

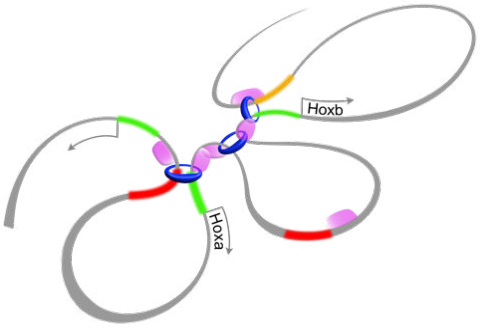






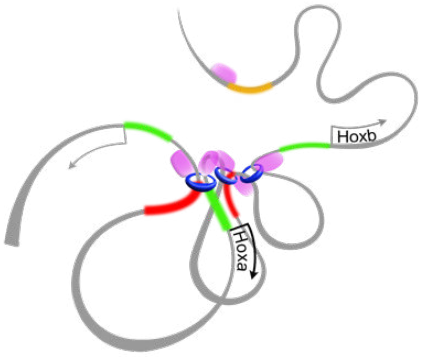






HoxB – loses contact with poised enhancers in distal genes

HoxA – gains contact with enhancers in distal genes



Organized as a gene cluster, the hox genes encode a conserved set of developmental transcription factors that specify body plan along the dorsal-ventral axis during embryogenesis. Dysregulation of developmental genes, like those at the hox loci has been linked to aging in yeast and mammals. Alteration of the enhancer interactome arising from DNA repair in the ICE mice results in hox gene misregulation and premature aging.